```
gaattcatctgtcgactgctaccacgggagtccccggagaaggatcctgcagcccgagt      60
cccgaggataaagcttggggttcatcctccctgatcctccacagtcctcaggct          120
tccccaatccaggggactcggcgccggacgctgctatggacgacattttcactcagtgc     180
                                        M   D   D   I   F   T   Q   C     8
CGGAGGGCAACGCCAGTCGCCGTTCGCCGTGGCTCGGCTGGCAGAACGACCTCAAC         240
  R   E   G   N   A   V   A   V   R   L   W   L   D   N   T   E   N   D   L   N      28
CAGGGGGACGATCATGGCTTCTCCCCTGCACTGGGGGGGCCGAGAGGGCCGCTCTGCT       300
  Q   G   D   D   H   G   F   S   P   L   H   W   A   C   R   E   G   R   S   A      48
GTGGTTGAGATGTTGATCATGCGGGGGCACGGATCAATGTAATGAACCCGTGGGATGAC     360
  V   V   E   M   L   I   M   R   G   A   R   I   N   V   M   N   R   G   D   D      68
ACCCCCCTGCATCTGGCAGCCAGTCATGGACACCGTGATATTGTACAGAAGCTATTGCAG     420
  T   P   L   H   L   A   A   S   H   G   H   R   D   I   V   Q   K   L   L   Q      88
TACAAGGCAGACATCAATGCAGTGAATGAACACGGGAATGTGCCCTGCACTATGCCTGT     480
  Y   K   A   D   I   N   A   V   N   E   H   G   N   V   P   L   H   Y   A   C     108
TTTTGGGGCCAAGATCAAGTGGCAGAGGACCTGGTGGCAAATGGGCCCTTGTCAGCATC     540
  F   W   G   Q   D   Q   V   A   E   D   L   V   A   N   G   A   L   V   S   I     128
TGTAACAAGTATGGAGAGATGCCTGTGGACGCACCCCTGAGAGAGCTTCTC             600
```
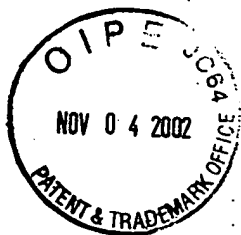
FIG. 1a (SEQ. ID. NO. 1)
(continued on page 4/23)

```
C  N  K  Y  G  E  M  P  V  D  K  A  K  A  P  L  R  E  L  L                                   148
CGAGAGCGGGCAGAGAAGATGGGCCAGAATCTCAACCGTATTCCATACAAGGACACATTC                                660
R  E  R  A  E  K  M  G  Q  N  L  N  R  I  P  Y  K  D  T  F                                   168
TGGAAGGGGACCACCCGCCACTCGGCCCCGAAATGGAACCCTGAACAAACACTCTGGCATT                               720
W  K  G  T  T  R  T  R  P  R  N  G  T  L  N  K  H  S  G  I                                   188
GACTTCAAACAGCTTAACTTCCTGACGAAGCTCAACGAGAATCACTCTGGAGAGCTATGG                                780
D  F  K  Q  L  N  F  L  T  K  L  N  E  N  H  S  G  E  L  W                                   208
AAGGGCCGCTGGCAGGGCAATGACATTGTCGTGAAGGTGCTGAGACTGGAGT                                        840
K  G  R  W  Q  G  N  D  I  V  V  K  V  L  K  V  R  D  W  S                                   228
ACAAGGAAGAGCAGGGACTTCAATGAAGAGTGTCCCCGGCTCAGGATTTTCTCGCATCCA                                900
T  R  K  S  R  D  F  N  E  E  C  P  R  L  R  I  F  S  H  P                                   248
AATGTGCTCCCAGTGCTAGGTGCTTGCCAGTCTCCACCTGCTCCTCCTACTCTCATC                                   960
N  V  L  P  V  L  G  A  C  Q  S  P  P  A  P  H  P  T  L  I                                   268
ACACACTGGATGCCGTATGGATCCCCTACAATTACTACATGAAGGCACCAATTTCGTC                                 1020
T  H  W  M  P  Y  G  S  L  Y  N  V  L  H  E  G  T  N  F  V                                   288
GTGGACCAGAGCCAGGCTGTGAAGTTTGCTTTGGACATGGCAAGGGGCATGGCCTTCCTA                               1080
V  D  Q  S  Q  A  V  K  F  A  L  D  M  A  R  G  M  A  F  L                                   308
CACACACTAGAGCCCCTCATCCCACGACATGCACTCAATAGCCGTAGTGTAATGATTGAT                               1140
H  T  L  E  P  L  I  P  R  H  A  L  N  S  R  S  V  M  I  D                                   328
```

FIG. 1a (SEQ. ID NO. 1)

```
GAGGACATGACTGCCCGAATTAGCATGGCTGATGTCAAGTTCTCTTTCCAATGTCCTGGT  1200
 E  D  M  T  A  R  I  S  M  A  D  V  K  F  S  F  Q  C  P  G    348
CGCATGTATGCACCTGCCTGGGTAGCCCCGGAAGCTCTGCAGAAGAAGCCTGAAGACACA  1260
 R  M  Y  A  P  A  W  V  A  P  E  A  L  Q  K  K  P  E  D  T    368
AACAGACGCTCAGCAGACATGTGGAGTTTTGCAGTGCTTCTGTGGGAACTGGTGACACGG  1320
 N  R  R  S  A  D  M  W  S  F  A  V  L  L  W  E  L  V  T  R    388
GAGGTACCCTTTGCTGACCTGTCCAATATGGAGATTGGAATGAAGGTGGCATTGGAAGGC  1380
 E  V  P  F  A  D  L  S  N  M  E  I  G  M  K  V  A  L  E  G    408
CTTCGGCCTACCATCCCACCAGGTATTCCCTCATGTGTAAGCTCATGAAGATCTGC      1440
 L  R  P  T  I  P  P  G  I  S  P  H  V  C  K  L  M  K  I  C    428
ATGAATGAAGACCCTGCAAAGCGACCCAAATTGACATGATTGTGCCTATCCTTGAGAAG   1500
 M  N  E  D  P  A  K  R  P  K  F  D  M  I  V  P  I  L  E  K    448
ATGCAGGACAAGtaggactggaggtcctgcctgactccagaggtgtcgggacatggt     1560
 M  Q  D  K  *
tgggggaatgcacctcccccaagcagcaggcctctggttgcctccccgcctccagtcat   1620
ggtactacccccagcctggggtccatcccctccccatccccactgtgcgcaagagg      1680
ggcgggctcagagctttgtcacttgccacatggtgtctccacatgggaggggatcagcc   1740
ccgcctgtcacaataaagtttattatgaaaaaaaaaaaaaaa                    1789
```

FIG. 1a (SEQ. ID. NO. 1)
continuation from page 3/23

3/23

```
                          I                     II

Csk    .NMKELKLLQ TIGKGEFGDV MLGDYRGN.K VAVKCIKNDA .TAQ....AF (SEQ. ID. NO. 15)
Yes    IPRESLRLEV KLGQGCFGEV WMGTWNGTTK VAIKTLKPGT MMPEAFLQ.. (SEQ. ID. NO. 4)
Ctrl   IPWCDLNIKE KIGAGSFGTV HRAEWHGS.D VAVKRILMEQD FHAE.RVNEF (SEQ. ID. NO. 5)
B-raf  IPDGQITVGQ RIGSGSFGTV YKGKWHG..D VAVKMLNVTA PTPQQ.LQAF (SEQ. ID. NO. 6)
Ilk    IDFKQLNFLT KLNENHSGEL WKGRWQGN.D IVVKVLDKVR DWSTRKSRDF (SEQ. ID. NO.16)


          III        IV                            V

Csk    LAEASVMTQ LRHSNLVQLL GVIVEE.KGG LYIVTEYMAK GSLVDYLRSR
Yes    ..EAQIMKK LRHDKLVPLY AVVSEE...P IYIVTEFMTK GSLLDFLKEG
Ctrl   LREVAIMKR LRHPNIVLFM GAVTQPP..N LSIVTEYLSR GSLYRLLHKS
B-raf  KNEVGVLRK TRHVNILLFM GYSTKP...Q LAIVTQWCEG SSLYHHLHII
Ilk    NEECPRLRI FSHPNVLPVL GACQSPPAPH PTLITHWMPY GSLYNVLHE.     283


                 VIa                    VIb

Csk    GRSV.LGGDC LLKFSLDVCE AMEYLEGN.. .NFVHRDLAA RNVLVS.E
Yes    EGKF.LKLPQ LVDMAAQIAD GMAYIERM.. .NYIHRDLRA ANILVG.D
Ctrl   GAREQLDERR RLSMAYDVAK GMNYLH.NRN PPIVHRDLKS PNLLV.DK
B-raf  ETKFEMI..K LIDIARQTAQ GMDYLHAK.. .SIIHRDLKS NNIFLH.E
Ilk    GTNFVVDQSQ AVKFALDMAR GMAFLH.TLE PLIPRHALNS RSVMI.DE     329
```

Fig. 1b

```
           VII                                                VIII
Csk    DNVAKVSDFG LTK.....EA SSTQDTGKLP VKWTAPEALR ...EKKFSTK  (SEQ. ID. NO. 15)
Yes    NLVCKIADFG LARLIED.NE YTARQGAKFP IKWTAPEAAL ...YGRFTIK  (SEQ. ID. NO. 4)
Ctrl   KYTVKVCDFG LSRLKAS.TF LSSKSAAGTP .EWMAPEVLR ...DEPSNEK  (SEQ. ID. NO. 5)
B-raf  DLTVKIGDFG LATVKSRWSG SHQFEQLSGS ILWMAPEVIR MQDKNPYSFQ  (SEQ. ID. NO. 6)
Ilk    DMTARIS... MADVKFSFQC PGRM.YA..P .AWVAPEALQ KKPEDTNRSS  (SEQ. ID. NO. 16)

           IX                          X
Csk    SDVWSFGILL WEIYSFGRVP YPRIPLKD.V VPRVEKGY.. KMDAPDGCPP
Yes    SDVWSFGILL TELVTKGRVP YPGMVNRE.V LEQVERGY.. RMPCPQGCPE
Ctrl   SDVYSFGVIL WELAT.LQQP WGNL.NPAQV VAAVGFKCK. RLEIPRNLNP
B-raf  SDVYAFGIVL YELMT.GQLP YSNINNRDQI IFMVGRGYLS PDLSKVRSNC
Ilk    ADMWSFAVLL WELVTR.EVP FADLSNMEIG MK.VALEGL. R.TIPPGISP   418

           XI
Csk    AVYEVMKN  CWHLDAAMRP SFLQLREQLE HIKTHEL
Yes    SLHELMKL  CWKKDPDERP TFEYIQSFLE ......
Ctrl   QVAAIIEG  CWTNEPWKRP SFATIMDLLR PL.....
B-raf  PKAMKRLMAECLKKKRDERP LFPQILASIE LLARSLP
Ilk    HVCKLMKI  CMNEDPAKRP KFDMIVPILE KMQDK..   451
```

Fig. 1b

ANKYRIN
CONSENSUS

-G-TPLH-AA--GH---V--LL--GA--N---- (SEQ. ID. NO. 17)
　　　　　　　A　　　　　　　D

ANK1　^{33}HGFSPLHWACREGRSAVVEMLIMRGARINVMNR (SEQ. ID. NO. 18)
ANK2　GDDTPLHLAASHGHRDIVQKLLQYKADINAVNE (SEQ. ID. NO. 19)
ANK3　HGNVPLHYACFWGQDQVAEDLVANGALVSICNK (SEQ. ID. NO. 20)
ANK4　YGEMPVDKAKAPLRELLRERAEKMGQNLNRIPY^{164}
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　(SEQ. ID. NO. 21)

Fig. 1c